

Gene Section

Mini Review

NKX2-2 (NK2 homeobox 2)

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Identity

Hugo: NKX2-2 Other names: NKX2.2; NKX2B Location: 20p11.22

DNA/RNA

Description

Start- 21,439,648 base pairs from p arm terminus; end-21,442,699 base pairs from p arm terminus; size- 3,051 bases; orientation- minus strand.

Protein

Description

273 amino acids; 30133 Da. NKX2-2 is a member of the NK2 family of homeobox transcription factors. It has known roles in the development of the CNS as well as pancreatic beta cell differentiation. In the CNS NKX2-2 is known to be activated by SHH signaling which is important for its initial role in ventral patterning. NKX2-2 expression has additionally been shown to be critical for the differentiation of oligodendrocytes, and in fact necessary for this process to occur. In both instances, NKX2-2 mediated transcripitional repression is both necessary and sufficient for these processes to occur. Regulation of NKX2-2 expression in the pancreas is less well understood. NKX2-2 knock-out mice die soon after birth from diabetic complications as a result of a lack of fully differentiated pancreatic beta cells. While NKX2-2 mediated transcriptional repression has been demonstrated to be necessary and sufficient for its role in beta-cell differentiation, it remains unclear whether NKX2-2 mediated transcriptional activation is important for NKX2-2 function in adult beta-cells.

Expression

V3 neural progenitors; oligodendrocyte precursor cells; precursor and adult pancreatic beta cells.

Localisation

Nuclear.

Function

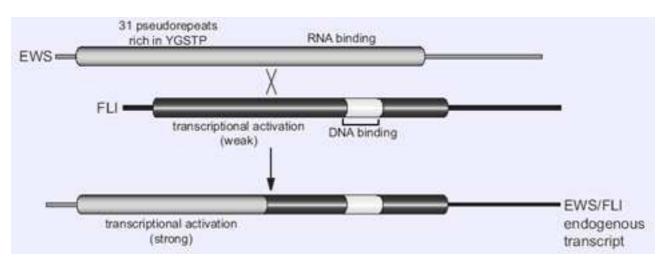
NKX2-2 is a transcription factor.

Homology

NKX2-2 shares homology with other members of the NK2 family of transcription factors most notably in the TN transcriptional repression, DNA binding homeodomain, and specific domain regions.



Schematic of NKX2-2 functional domains. The positions of the transcriptional repressor domain (TN), the homeodomain (HD), the NK2-specific domain (SD), and the transcriptional activation domain (TAD) are shown.



Schematic diagram of wild-type EWS, wild-type FLI, and the EWS/FLI fusion transcripts.

Implicated in

Ewing's sarcoma

Prognosis

Roughly 50% survival at 5 years for Ewing's sarcoma. **Cytogenetics**

Ewing's sarcoma cells harbor the characteristic translocation t(11;22)(q24;q12) in roughly 90% of cases.

Hybrid/Mutated Gene

t(11;22)(q24;q12) fuses the 5' region of the EWSR1 gene on chromosome 22 with the 3' portion of the FLI-1 gene on chromosome 11.

Abnormal Protein

The translocation fusion product is termed EWS/FLI. **Oncogenesis**

NKX2-2 is up-regulated in Ewing's sarcoma by the EWS/FLI translocation protein product. NKX2.2 expression is necessary for the oncogenic phenotype of Ewing's sarcoma cells.

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